

McElwain

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/219,935

DATE: 05/05/1999
TIME: 15:17:51

INPUT SET: S31737.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Browse, John, Kinney, Anthony J.,
6 Pierce, John, Wierzbicki, Anna M.,
7 Yadav, Narendra S., Perez-Grau, Luis
8
9 (ii) TITLE OF INVENTION: Fatty Acid Desaturase Genes
10 from Plants
11
12 (iii) NUMBER OF SEQUENCES: 32
13
14 (iv) CORRESPONDENCE ADDRESS:
15
16 (A) ADDRESSEE: E. I. du Pont de Nemours and Company
17 (B) STREET: 1007 Market Street
18 (C) CITY: Wilmington
19 (D) STATE: Delaware
20 (E) COUNTRY: U.S.A.
21 (F) ZIP: 19898
22
23 (v) COMPUTER READABLE FORM:
24
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: Macintosh
27 (C) OPERATING SYSTEM: Macintosh System, 6.0
28 (D) SOFTWARE: Microsoft Word, 4.0
29
30 (vi) CURRENT APPLICATION DATA:
31
32 (A) APPLICATION NUMBER: 09/219,935
33 (B) FILING DATE:
34 (C) CLASSIFICATION:
35
36 (vii) PRIOR APPLICATION DATA:
37
38 (A) APPLICATION NUMBER: 08/244,205
39 (B) FILING DATE:
40
41 (viii) ATTORNEY/AGENT INFORMATION:
42
43 (A) NAME: Floyd, Linda A.
44 (B) REGISTRATION NUMBER: 33,692
45 (C) REFERENCE/DOCKET NUMBER: BB-1036-A
46

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47 (ix) TELECOMMUNICATION INFORMATION:

48

49 (A) TELEPHONE: (302) 992-4929

50 (B) TELEFAX: (302) 892-7949

51 (C) TELEX: 835420

52

53

54 (2) INFORMATION FOR SEQ ID NO:1:

55

56 (i) SEQUENCE CHARACTERISTICS:

57

58 (A) LENGTH: 1350 base pairs

59 (B) TYPE: nucleic acid

60 (C) STRANDEDNESS: single

61 (D) TOPOLOGY: linear

62

63 (ii) MOLECULE TYPE: cDNA

64

65 (iii) HYPOTHETICAL: NO

66

67 (vi) ORIGINAL SOURCE:

68

69 (A) ORGANISM: Arabidopsis thaliana

70

71 (vii) IMMEDIATE SOURCE:

72

73 (B) CLONE: pCF3

74

75 (ix) FEATURE:

76

77 (A) NAME/KEY: CDS

78 (B) LOCATION: 46..1206

79

80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

81

82 CTCTCTCTCT CTCTCTTCTC TCTTTCTCTC CCCCTCTCTC CGGCG ATG GTT GTT 54

83 Met Val Val

84 1

85

86 GCT ATG GAC CAA CGC ACC AAT GTG AAC GGA GAT CCC GGC GCC GGA GAC 102

87 Ala Met Asp Gln Arg Thr Asn Val Asn Gly Asp Pro Gly Ala Gly Asp

88 5 10 15

89

90 CGG AAG AAA GAA GAA AGG TTT GAT CCG AGT GCA CAA CCA CCG TTC AAG 150

91 Arg Lys Lys Glu Glu Arg Phe Asp Pro Ser Ala Gln Pro Pro Phe Lys

92 20 25 30 35

93

94 ATC GGA GAT ATA AGG GCG GCG ATT CCT AAG CAC TGT TGG GTT AAG AGT 198

95 Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp Val Lys Ser

96 40 45 50

97

98 CCT TTG AGA TCA ATG AGT TAC GTC GTC AGA GAC ATT ATC GCC GTC GCG 246

99 Pro Leu Arg Ser Met Ser Tyr Val Val Arg Asp Ile Ile Ala Val Ala

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	55	60	65	
100				
101				
102	GCT TTG GCC ATC GCT GCC GTG TAT GTT GAT AGC TGG TTC CTT TGG CCT			294
103	Ala Leu Ala Ile Ala Ala Val Tyr Val Asp Ser Trp Phe Leu Trp Pro			
104	70	75	80	
105				
106	CTT TAT TGG GCC GCC CAA GGA ACA CTT TTC TGG GCC ATC TTT GTT CTC			342
107	Leu Tyr Trp Ala Ala Gln Gly Thr Leu Phe Trp Ala Ile Phe Val Leu			
108	85	90	95	
109				
110	GGC CAC GAC TGT GGA CAT GGG AGT TTC TCA GAC ATT CCT CTA CTG AAT			390
111	Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro Leu Leu Asn			
112	100	105	110	115
113				
114	AGT GTG GTT GGT CAC ATT CTT CAT TCT TTC ATC CTC GTT CCT TAC CAT			438
115	Ser Val Val Gly His Ile Leu His Ser Phe Ile Leu Val Pro Tyr His			
116	120	125	130	
117				
118	GGT TGG AGA ATA AGC CAC CGG ACA CAC CAC CAG AAC CAT GGC CAT GTT			486
119	Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His Gly His Val			
120	135	140	145	
121				
122	GAA AAC GAC GAG TCA TGG GTT CCG TTA CCA GAA AGG GTG TAC AAG AAA			534
123	Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Arg Val Tyr Lys Lys			
124	150	155	160	
125				
126	TTG CCC CAC AGT ACT CGG ATG CTC AGA TAC ACT GTC CCT CTC CCC ATG			582
127	Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro Leu Pro Met			
128	165	170	175	
129				
130	CTC GCA TAT CCT CTC TAT TTG TGC TAC AGA AGT CCT GGA AAA GAA GGA			630
131	Leu Ala Tyr Pro Leu Tyr Leu Cys Tyr Arg Ser Pro Gly Lys Glu Gly			
132	180	185	190	195
133				
134	TCA CAT TTT AAC CCA TAC AGT AGT TTA TTT GCT CCA AGC GAG AGA AAG			678
135	Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser Glu Arg Lys			
136	200	205	210	
137				
138	CTT ATT GCA ACT TCA ACT ACT TGT TGG TCC ATA ATG TTC GTC AGT CTT			726
139	Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Phe Val Ser Leu			
140	215	220	225	
141				
142	ATC GCT CTA TCT TTC GTC TTC GGT CCA CTC GCG GTT CTT AAA GTC TAC			774
143	Ile Ala Leu Ser Phe Val Phe Gly Pro Leu Ala Val Leu Lys Val Tyr			
144	230	235	240	
145				
146	GGT GTA CCG TAC ATT ATC TTT GTG ATG TGG TTG GAT GCT GTC ACG TAT			822
147	Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala Val Thr Tyr			
148	245	250	255	
149				
150	TTG CAT CAT CAT GGT CAC GAT GAG AAG TTG CCT TGG TAT AGA GGC AAG			870
151	Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr Arg Gly Lys			
152	260	265	270	275

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153
154 GAA TGG AGT TAT CTA CGT GGA GGA TTA ACA ACA ATT GAT AGA GAT TAC 918
155 Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp Arg Asp Tyr
156 280 285 290
157
158 GGA ATC TTT AAC AAC ATT CAT CAC GAC ATT GGA ACT CAC GTG ATC CAT 966
159 Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His Val Ile His
160 295 300 305
161
162 CAT CTC TTC CCA CAA ATC CCT CAC TAT CAC TTG GTC GAC GCC ACG AAA 1014
163 His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp Ala Thr Lys
164 310 315 320
165
166 GCA GCT AAA CAT GTG TTG GGA AGA TAC TAC AGA GAA CCA AAG ACG TCA 1062
167 Ala Ala Lys His Val Leu Gly Arg Tyr Tyr Arg Glu Pro Lys Thr Ser
168 325 330 335
169
170 GGA GCA ATA CCG ATC CAC TTG GTG GAG AGT TTG GTC GCA AGT ATT AAG 1110
171 Gly Ala Ile Pro Ile His Leu Val Glu Ser Leu Val Ala Ser Ile Lys
172 340 345 350 355
173
174 AAA GAT CAT TAC GTC AGC GAC ACT GGT GAT ATT GTC TTC TAC GAG ACA 1158
175 Lys Asp His Tyr Val Ser Asp Thr Gly Asp Ile Val Phe Tyr Glu Thr
176 360 365 370
177
178 GAT CCA GAT CTC TAC GTT TAC GCT TCT GAC AAA TCT AAA ATC AAT TAATCTCCAT 1213
179 Asp Pro Asp Leu Tyr Val Tyr Ala Ser Asp Lys Ser Lys Ile Asn
180 375 380 385
181
182 TTGTTTAGCT CTATTAGGAA TAAACCAGCC CACTTTTAAA ATTTTATTT CTTGTTGTTT 1273
183
184 TTAAGTTAAA AGTGACTCG TGAACTCTT TTTTTTTCT TTTTTTTAT TAATGTATTT 1333
185
186 ACATTACAAG GCGTAAA 1350
187
188
189 (2) INFORMATION FOR SEQ ID NO:2:
190
191 (i) SEQUENCE CHARACTERISTICS:
192
193 (A) LENGTH: 386 amino acids
194 (B) TYPE: amino acid
195 (D) TOPOLOGY: linear
196
197 (ii) MOLECULE TYPE: protein
198
199 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
200
201 Met Val Val Ala Met Asp Gln Arg Thr Asn Val Asn Gly Asp Pro Gly
202 1 5 10 15
203
204 Ala Gly Asp Arg Lys Lys Glu Glu Arg Phe Asp Pro Ser Ala Gln Pro
205 20 25 30

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206
207 Pro Phe Lys Ile Gly Asp Ile Arg Ala Ala Ile Pro Lys His Cys Trp
208           35                      40                      45
209
210 Val Lys Ser Pro Leu Arg Ser Met Ser Tyr Val Val Arg Asp Ile Ile
211     50                      55                      60
212
213 Ala Val Ala Ala Leu Ala Ile Ala Ala Val Tyr Val Asp Ser Trp Phe
214   65                      70                      75                      80
215
216 Leu Trp Pro Leu Tyr Trp Ala Ala Gln Gly Thr Leu Phe Trp Ala Ile
217           85                      90                      95
218
219 Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser Asp Ile Pro
220           100                      105                      110
221
222 Leu Leu Asn Ser Val Val Gly His Ile Leu His Ser Phe Ile Leu Val
223           115                      120                      125
224
225 Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His Gln Asn His
226   130                      135                      140
227
228 Gly His Val Glu Asn Asp Glu Ser Trp Val Pro Leu Pro Glu Arg Val
229  145                      150                      155                      160
230
231 Tyr Lys Lys Leu Pro His Ser Thr Arg Met Leu Arg Tyr Thr Val Pro
232           165                      170                      175
233
234 Leu Pro Met Leu Ala Tyr Pro Leu Tyr Leu Cys Tyr Arg Ser Pro Gly
235           180                      185                      190
236
237 Lys Glu Gly Ser His Phe Asn Pro Tyr Ser Ser Leu Phe Ala Pro Ser
238           195                      200                      205
239
240 Glu Arg Lys Leu Ile Ala Thr Ser Thr Thr Cys Trp Ser Ile Met Phe
241   210                      215                      220
242
243 Val Ser Leu Ile Ala Leu Ser Phe Val Phe Gly Pro Leu Ala Val Leu
244  225                      230                      235                      240
245
246 Lys Val Tyr Gly Val Pro Tyr Ile Ile Phe Val Met Trp Leu Asp Ala
247           245                      250                      255
248
249 Val Thr Tyr Leu His His His Gly His Asp Glu Lys Leu Pro Trp Tyr
250           260                      265                      270
251
252 Arg Gly Lys Glu Trp Ser Tyr Leu Arg Gly Gly Leu Thr Thr Ile Asp
253           275                      280                      285
254
255 Arg Asp Tyr Gly Ile Phe Asn Asn Ile His His Asp Ile Gly Thr His
256   290                      295                      300
257
258 Val Ile His His Leu Phe Pro Gln Ile Pro His Tyr His Leu Val Asp

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SEQUENCE VERIFICATION REPORT
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Original Text